

10_578839 sequence listing (Q94769).TXT
SEQUENCE LISTINGS

<110> INJE UNIVERSITY
<120> CANCER CELL TARGETING GENE DELIVERY METHOD
<130> Q94769
<140> US 10/578,839
<141> 2006-05-10
<150> KR 10-2003-0079897
<151> 2003-11-12
<150> PCT/KR2004/000545
<151> 2004-03-15
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<211> 36
<212> DNA
<213> Artificial Sequence
<220>
<223> Env F primer

<400> 1
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<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> 597LN primer

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<211> 49
<212> DNA
<213> Artificial Sequence
<220>
<223> LC597 primer

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<210> 4
<211> 35
<212> DNA

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<213> Artificial Sequence

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<223> Spike R2 primer

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<211> 36

<212> DNA

<213> Artificial Sequence

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<223> LnkNScFv primer

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<211> 36

<212> DNA

<213> Artificial Sequence

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<223> ScFvLnkC primer

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<210> 7

<211> 2058

<212> DNA

<213> Gibbon Ape leukemia virus

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<222> (1)..(126)

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<221> misc_feature

<222> (127)..(1467)

<223> surface subunit region

<220>

<221> misc_feature

<222> (1468)..(2025)

<223> transmembrin domain

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gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcagggtactg 180

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tcccaaactg	gagacgttgt	ctgggataca	aaggcagtcc	agcccccttg	gacttggtgg	240
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<210> 8
 <211> 786
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (346)..(390)
 <223> (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (739)..(777)
 <223> PreS1 Tag

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 cctggacaac gccttgagtg gatgggatat ttttctcctg gcaacgatga ttttaaatac 180
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<210> 9
 <211> 13
 <212> PRT
 <213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
 1 5 10

<210> 10
 <211> 2871
 <212> DNA

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<213> Artificial Sequence

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<223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

<400> 10

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gcaagctcta ctttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
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gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta 1560
cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc 1620
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ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
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<210> 11
<211> 956
<212> PRT
<213> Artificial Sequence

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<220>
<223> ScFv-GaLV Env GP chimeric ligand (FVGEL199)

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Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
          20           25           30
Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
          35           40           45
Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
          50           55           60

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Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
65      70      75      80
Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
      85      90
Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
      100      105      110
Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
      115      120      125
Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
      130      135      140
Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
      145      150      155      160
Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
      165      170      175
Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
      180      185      190
Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
      195      200      205
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
      210      215      220
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
      225      230      235      240
Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
      245      250      255
Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
      260      265      270
Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
      275      280      285
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
      290      295      300
Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
      305      310      315      320
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
      325      330      335
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
      340      345      350
Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
      355      360      365
Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
      370      375      380
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
      385      390      395      400

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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 405 410 415
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
 420 425 430
 Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala
 435 440 445
 Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
 450 455 460
 Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
 465 470 475 480
 Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
 485 490 495
 Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
 500 505 510
 Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
 515 520 525
 Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
 530 535 540
 Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
 545 550 555 560
 Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
 565 570 575
 Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
 580 585 590
 Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
 595 600 605
 Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
 610 615 620
 Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
 625 630 635 640
 ser ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
 645 650 655
 Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
 660 665 670
 Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
 675 680 685
 Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
 690 695 700
 His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
 705 710 715 720
 Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
 725 730 735

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Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
740 745 750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
755 760 765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
770 775 780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785 790 795 800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
805 810 815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
820 825 830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
835 840 845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
850 855 860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865 870 875 880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
885 890 895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
900 905 910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
915 920 925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
930 935 940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945 950 955